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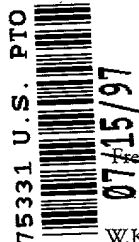
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July 14, 1997

Attorney Docket No.: 04599/005001

**BOX PATENT APPLICATION**

Assistant Commissioner of Patents  
Washington, DC 20231

Presented for filing is a new original patent application of:

**Applicant:** SCOTT W. VAN ARSDELL, R. ROGERS YOCUM,  
JOHN B. PERKINS, and JANICE G. PERO  
**Title :** OVERCOMING DAPA AMINOTRANSFERASE  
BOTTLENECKS IN BIOTIN VITAMERS BIOSYNTHESIS

Enclosed are the following papers, including all those required for a filing date under 37 CFR §1.53(b):

Pages of Specification	24
Pages of Claims	4
Pages of Abstract	1
Signed Declaration	[To Be Filed At A Later Date]
Sheets of Drawing	4

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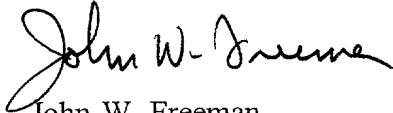
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Respectfully submitted,

A handwritten signature in black ink, appearing to read "John W. Freeman". The signature is fluid and cursive, with the first name "John" being the most prominent part.

John W. Freeman  
Reg. No. 29,066

617-542-5070

**APPLICATION**  
**FOR**  
**UNITED STATES LETTERS PATENT**

**TITLE:** OVERCOMING DAPA AMINOTRANSFERASE BOTTLENECKS  
IN BIOTIN VITAMERS BIOSYNTHESIS

**APPLICANT:** SCOTT W. VAN ARSDELL, R. ROGERS YOCUM, JOHN B.  
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OVERCOMING DAPA AMINOTRANSFERASE  
BOTTLENECKS IN BIOTIN VITAMERS BIOSYNTHESIS

5                   Background of the Invention

The present invention is in the general field of the biosynthesis of biotin vitamers.

634633  
Biotin biosynthesis in *Escherchia coli* and *Bacillus sphaericus* has been studied at both the biochemical and  
10 molecular biological levels (DeMoll, 1996. In F.C. Neidhardt et al., (eds.) *E. coli* and *Salmonella typhimurium*: Cellular and Molecular Biology, Second edition ed., vol 1., pp. 704-709, ASM Press, Washington, D.C.; Perkins et al., In A.L. Sonenshein et al. (eds.), *In Bacillus subtilis* and  
15 Other Gram Positive Bacteria: Biochemistry, Physiology, and Molecular Genetics, pp. 319-334, American Society for Microbiology, Washington, D.C.; Eisenberg, 1987. In F. Neidhardt et al. (eds.), *E. coli* and *Salmonella typhimurium*, pp. 544-550. American Society for Microbiology, Washington,  
20 D.C.; Cronan, Cell 58:427-429, 1989, Izumi et al., Agric. Biol. Chem. 45:1983-1989, 1981; Gloeckler et al., Gene 87:63-70, 1990), although some steps and components in biotin synthesis remain to be elucidated (Ohshiro et al., Biosci. Biotech. Biochem. 58:1738-1741, 1994; Ifuku et al.,  
25 Eur. J. Biochem. 224:173-178, 1994; Florentin et al., C.R. Acad. Sci. Paris 317:485-488, 1994; Birch et al., J. Biol. Chem. 270:19158-19165, 1995; Sanyal et al., Biochemistry 33:3625-3631, 1995). Several enzymes involved in the conversion of pimeloyl-CoA to biotin have been isolated and  
30 characterized from both of these bacterial species (Ploux et al., Biochem. J. 283:327-321, 1992; Izumi et al., Agric. Biol. Chem. 45:1983-1989, 1981; Eisenberg, *supra*, Huang et al., Biochemistry 34:10985-10995, 1995). KAPA synthase, the product of *bioF*, catalyzes the conversion of pimeloyl-CoA

and alanine to 8-amino-7-ketopelargonic acid (KAPA). DAPA  
aminotransferase, the product of *bioA*, then transfers an  
amino group from a donor to KAPA yielding 7,8-  
diaminopelargonic acid (DAPA). Dethiobiotin synthetase  
5 (*bioD*) catalyzes the closure of the ureido-ring to produce  
dethiobiotin (DTB), and finally the product of *bioB*, biotin  
synthase, functions together with a number of other  
components including flavodoxin (Birch et al., *supra*; Ifuku  
et al., *supra*) S-adenosylmethionine (SAM) (Florentin, C.R.  
10 Acad. Sci. Paris 317:485-488, 1994; Ohshiro et al., *supra*;  
Sanyal et al., *supra*; Birch et al., *supra*) ferredoxin NADP<sup>+</sup>  
reductase (Birch et al., *supra*; Sanyal et al., Arch.  
Biochem. Biophys. 326:48-56, 1996) and possibly cysteine  
(Florentin, C.R. Acad. Sci. Paris 317:485-488, 1994; Birch  
15 et al., *supra*; Sanyal et al., *supra*) to convert dethiobiotin  
to biotin. The compounds KAPA, DAPA, DTB, and biotin are  
collectively or singly referred to as vitamers or biotin  
vitamers.

In *E. coli* the genes that encode these enzymes are  
20 located in two divergently transcribed operons, controlled  
by a single operator that interacts with the BirA repressor  
(Cronan, Cell 58:427-429, 1989). In *B. sphaericus*, the  
genes are located in two separate operons (Gloeckler et al.,  
*supra*. The early steps of the pathway, those involved in  
25 the synthesis of pimeloyl-CoA, are less well understood  
(Ifuku et al., Eur. J. Biochem. 224:173-178, 1994; Sanyal et  
al., J. Am. Chem. Soc. 116:2637-2638, 1994). *B. sphaericus*  
contains an enzyme, pimeloyl-CoA synthetase (*bioW*) that  
converts pimelic acid to pimeloyl CoA (Gloeckler et al.,  
30 Gene 87:63-70, 1990), (Ploux et al., Biochem. J. 287:685-  
690, 1992). *E. coli* lacks this enzyme and cannot use  
pimelic acid as an intermediate in biotin synthesis  
(Gloeckler et al., *supra*; Ifuku et al., Eur. J. Biochem.

224:173-178, 1994; Sanyal et al., J. Am. Chem. Soc.  
116:2637-2638, 1994). *E. coli* contains two genes, *bioC*  
which is located in the *bio* operon and *bioH* which is  
unlinked to the other *bio* genes, that both appear to be  
5 involved in the early steps of biotin biosynthesis leading  
up to pimeloyl-CoA, but their exact roles are unknown  
(Eisenberg, *supra*; Lemoine et al., Mol. Micro. 19:645-647,  
1996).

*B. subtilis* contains homologs of the *E. coli* and *B.*  
10 *sphaericus* *bioA*, *bioB*, *bioD*, and *bioF* genes. These four  
genes along with a homolog of the *B. sphaericus* *bioW* gene  
are arranged in a single operon in the order *bioWAFDB*, and  
are followed by two additional genes, *bioI* and *orf2* (Bower  
et al., J. Bacteriol. 178:4122-4130, 1996). *bioI* and *orf2*  
15 are generally dissimilar to other known biotin biosynthetic  
genes. The *bioI* gene encodes a protein with similarity to  
cytochrome P450s and is able to complement mutations in  
either *E. coli* *bioC* or *bioH* (Bower et al., *supra*. Mutations  
in *bioI* cause *B. subtilis* to grow poorly in the absence of  
20 biotin. The bradytroph phenotype of *bioI* mutants can be  
overcome by pimelic acid, suggesting that the product of  
*bioI* functions at a step prior to pimelic acid synthesis  
(Bower et al., *supra*).

The *B. subtilis* *bio* operon is preceded by a putative  
25 vegetative promoter sequence and contains, just downstream,  
a region of dyad symmetry with homology to the *bio*  
regulatory region of *B. sphaericus* (Bower et al., *supra*.  
Analysis of a *bioW-lacZ* translational fusion indicates that  
expression of the biotin operon is regulated by biotin and  
30 the *B. subtilis* *birA* gene. Strains deregulated for biotin  
synthesis can be engineered by replacing the promoter and  
regulatory region with a constitutive promoter as described  
in European Patent Application 0635572 A2, incorporated

herein by reference. Production of biotin and biotin  
vitamers can be further improved by integration and  
amplification of the deregulated genes in the *B. subtilis*  
chromosome. Strain BI282, in European Patent Application  
5 0635572 A2, herein incorporated by reference, is an example  
of such a strain.

### Summary of the Invention

We have found that the conversion of KAPA to DAPA  
is a serious bottleneck in the biosynthesis of biotin using  
10 engineered cells that are fed pimelic acid. As other  
controls on biotin biosynthesis are removed, the KAPA to  
DAPA conversion is unable to keep pace with KAPA production,  
resulting in a build-up of KAPA, without a concomitant  
increase in the final product. We have also discovered that  
15 an important component of the bottleneck is the availability  
and identity of the amino donor used in the KAPA to DAPA  
conversion. In general, providing adequate quantities of  
the amino donor is an important strategy for overcoming the  
bottleneck. Moreover, a DAPA aminotransferase able to use  
20 lysine and related compounds as a source of the amino group  
to be transferred in the reaction which produces DAPA from  
KAPA, can significantly improve biosynthetic yields of the  
downstream biotin vitamers, especially dethiobiotin (DTB).

Although we do not wish to be limited to one  
25 specific explanation for our finding to the exclusion of  
other factors, it appears that providing higher levels of an  
amino donor which can be used by the available  
aminotransferase substantially ameliorates the bottleneck  
discussed above. For example, bacterial production of the  
30 biotin vitamers by bacteria whose DAPA aminotransferase uses  
lysine as an amino donor can be dramatically improved by  
making sufficient lysine available, either by including it

in the fermentation medium or by deregulating the lysine biosynthetic pathway. Such a strategy can also be applied to the use of DAPA aminotransferases of *B. subtilis* and close relatives, including members of the cluster of  
5 *Bacillus* spp. represented by *B. subtilis*. The cluster includes, e.g., *B. subtilis*, *B. pumilus*, *B. licheniformis*, *B. amyloliquefaciens*, *B. megaterium*, *B. cereus* and *B. thuringiensis*. The members of the *B. subtilis* cluster are genetically and metabolically divergent from the more  
10 distantly related *Bacillus* spp. of clusters represented by *B. sphaericus* and *B. stearothermophilus* (Priest, *In Bacillus subtilis* and Other Gram-Positive Bacteria, *supra* pp. 3-16, hereby incorporated by reference; Stackebrand, et al. *J. Gen. Micro.* 133:2523-2529, 1987, hereby incorporated by  
15 reference).

Accordingly, one aspect of the invention generally features a method of biosynthesizing (e.g., enzymatically or in fermentations using engineered cells) a biotin vitamer by culturing a bacterium that includes a lysine-utilizing DAPA  
20 aminotransferase in an environment enriched in lysine, lysine precursor(s), or analog(s). The desired biotin vitamer is then recovered from the environment. The ability of an amino donor to be used with a given aminotransferase may be evaluated in any appropriate assay, including but not  
25 limited to a bioassay based on that described by Eisenberg and Stoner (1971, *infra*) in which a DAPA sensitive strain of *E. coli* is used to measure DAPA aminotransferase activity. Typically, the bacterium will also be deregulated with respect to one or more biotin synthetic pathway steps, e.g.,  
30 as described in EP 635572, incorporated above. The DAPA aminotransferase may be produced by the cell's wild-type genetic material, by exogenous nucleic acid introduced into the cell, or both.



As used herein, a "lysine-utilizing DAPA aminotransferase" means a DAPA aminotransferase capable of converting 8-amino-7-ketopelargonic acid (KAPA) to diaminopelargonic acid (DAPA) utilizing lysine or a compound that is converted to lysine or a compound that can substitute for lysine as the amino donor.

As used herein, an "environment enriched for" means a bacterial culture in which the concentration of the indicated molecule is greater than that found under standard culture conditions, and greater than is necessary to avoid limiting cell growth in the absence of biotin vitamer overproduction.

The biotin vitamer product to be recovered and purified can be biotin, dethiobiotin, or diaminopelargonic acid (DAPA). When dethiobiotin or DAPA is recovered, the method may further include the step of converting the recovered dethiobiotin or DAPA to biotin.

In another aspect of the invention a bacterial strain is also engineered to overcome the KAPA-to-DAPA bottleneck by overproducing a DAPA aminotransferase capable of transferring an amino group from an amino donor to 8-amino-7-ketopelargonic acid (KAPA). In a preferred embodiment of this aspect of the invention, the bacterial strain is further engineered to overproduce the biotin vitamer by deregulation of a biotin biosynthetic step other than the KAPA-DAPA step.

To further circumvent the KAPA-to-DAPA bottleneck, the strain may be further engineered to produce multiple DAPA-aminotransferases, relying on different amino donors (e.g., lysine and SAM). These activities may be assayed and distinguished as described in detail below. Briefly, the level of KAPA-to-DAPA conversion may be measured by vitamer bioassays and bioautography of products from bacteria grown

in the presence of lysine, methionine, or lysine and methionine.

As used herein, "SAM-utilizing DAPA amino transferase" means a DAPA aminotransferase capable of  
5 converting 8-amino-7-ketopelargonic acid (KAPA) to diaminopelargonic acid (DAPA) utilizing S-adenosylmethionine (SAM) or a compound that is converted to SAM or a compound that can substitute for SAM as the amino donor.

In other embodiments, methionine and lysine, or  
10 their analogs are added to the medium.

One way to provide a lysine-rich environment is to enrich the culture with lysine or a lysine homolog that can donate an amino group to KAPA in the DAPA aminotransferase reaction. Lysine homologs include lysine, (S)-2-aminoethyl-  
15 L-cysteine (AEC) and other lysine homologs that can serve as amino donors for a DAPA aminotransferase. Another way to provide a lysine-rich environment is to deregulate the bacterium with respect to lysine production by mutating or engineering it to significantly reduce wild-type control  
20 over lysine production. For example, deregulation of a lysine synthetic step includes reducing or removing regulation of transcriptional or other expressional control of a lysine synthetic enzyme, or modification of a lysine synthetic enzyme to reduce or remove control over lysine  
25 biosynthesis. Deregulation also includes overproducing compounds which are starting materials in the lysine synthetic pathway, and inhibiting biodegradation of lysine (Amino Acids: Biosynthesis and Genetic Regulations, E. Hermann and R. Somerville (eds.) Addison Wesley, Reading, MA  
30 1983, pp. 147-172, 213-244, 417).

Deregulation of a biotin synthetic step includes reducing or removing regulation of transcriptional or other expressional control of a biotin synthetic enzyme, or

modification of a biotin synthetic enzyme to reduce or  
remove control over the enzyme-catalyzed biotin synthetic  
reaction. It can also include overproducing compounds which  
are starting materials in the biotin synthetic pathway, and  
5 inhibiting biodegradation of a desired biotin vitamer.

Bacteria can be engineered by intentionally and  
specifically altering the wild-type genome to produce a  
desired biosynthetic phenotype -- e.g., to synthesize more  
lysine than the corresponding wild-type, unengineered  
10 organism, or to remove a bottleneck in the biotin  
biosynthetic pathway.

Conversion of DTB to biotin may be by any means  
including but not limited to biochemical conversion of DTB  
to biotin, feeding DTB to bacteria engineered for the  
15 bioconversion of DTB to biotin (Fujisawa et al., Biosci.  
Biotech. Biochem. 57:740-744, 1993), *in vitro* synthesis of  
biotin from DTB (Birch et al., J. Biol. Chem. 270:19158-  
19165, 1995; Fujisawa et al., FEMS Microbiology Letters  
110:1-4, 1993; Ifuku et al., Biosci. Biotech. Biochem.  
20 56:1780-1785, 1992; Birch, WO 94/08023) or chemical  
synthesis.

#### Brief Description of the Drawings

Figure 1 is a representation of data showing the  
effect of KAPA concentration on *B. subtilis* DAPA  
25 aminotransferase activity.

Figure 2 is a reciprocal plot of initial velocity  
data for *B. subtilis* DAPA aminotransferase in the presence  
of varying concentrations of KAPA.

Figure 3 is a representation of results from a  
30 bioautography of fermentation broths of different bacterial  
strains with lysine and methionine or with or without  
lysine, as described in Table 5.

Figure 4 is a diagram of the *B. subtilis* biosynthetic pathway for lysine and related compounds.

#### Description of Tables

Table 1 is a representation of the data of a DAPA aminotransferase assay of an extract of BI611 by addition of potential amino donors to the reaction mix.

Table 2 is a representation of the results of a DAPA aminotransferase assay of an extract of BI611 after addition of lysine or lysine-related compounds to the reaction mix.

Table 3 is a representation of biotin and vitamer production of BI282 and BI603 grown in bench scale fermenters in the presence of 6 g lysine/liter.

Table 4 is a representation of biotin and vitamer production of BI282, BI96, and BI90 grown in bench scale fermentors in the presence of 3 g methionine/liter in the batch and feed.

Table 5A-5B represents biotin and vitamer production from strains BI603 and BI90 grown in bench scale fermentors in the presence or absence of 6 g lysine/liter and 3 g methionine/liter.

Table 6 is a representation of results of an assay of biotin and vitamer production using different lysine feed regimens.

Table 7 lists known *B. subtilis* lysine-deregulated mutants.

Table 8 is a representation of results of an assay of biotin and vitamer production of bacterial strains resistant to AEC grown in the presence of pimelic acid.

Appendix I describes a composition of medium for biotin and vitamer production in bench scale fermentors.

Appendix II describes an avidin-HABA displacement assay for biotin and DTB.

### Description of the Preferred Embodiments

A bottleneck in KAPA-to-DAPA conversion occurs during pimelic acid-fed fermentations of *B. subtilis*. In the experiments described below, we discovered that in *B. subtilis*, DAPA aminotransferase uses lysine as an amino donor, in contrast to S-adenosylmethionine (SAM), the compound that serves as the amino donor for DAPA aminotransferases of *B. sphaericus* (Izumi et al., Agric. Biol. Chem. 45:1983-1989, 1981), *Brevibacterium divaricatum*, *Salmonella typhimurium*, *Aerobacter aerogenes*, *Bacillus roseus*, *Micrococcus roseus*, and *Sarcina marginata* (Izumi et al., Agr. Biol. Chem. 39:175-181, 1975), *E. coli* (Eisenberg et al., J. Bacteriol. 108:1135-1140, 1971), and *S. marcescens*.

In *E. coli* and *B. sphaericus*, the conversion of KAPA to DAPA is catalyzed by DAPA aminotransferase, the product of the *bioA* gene, which utilizes SAM and KAPA as substrates (Eisenberg et al., J. Bacteriol. 108:1135-1140, 1971; Izumi et al., Agric. Biol. Chem. 45:1983-1989, 1981; Stoner et al., J. Biol. Chem. 250:4037-4043, 1975; Stoner et al., J. Biol. Chem. 250:4029-4036). It had been assumed that the reaction was similar in *B. subtilis* since the *B. subtilis* aminotransferase is 33% homologous with the *E. coli* enzyme and can complement *bioA* mutants in *E. coli*. However, *in vitro* assays of the *B. subtilis* enzyme led to our surprising discovery that lysine is an amino donor for the *B. subtilis* DAPA aminotransferase. Furthermore, the addition of lysine (2-10 g/l) to the fermentation medium of *B. subtilis* biotin production strains such as BI282 reduced the amount of KAPA produced and led to the accumulation of significant quantities of dethiobiotin (DTB). Various fermentative or chemical methods can then be used to convert DTB to biotin.

The observation that SAM was not a significant amino donor for the *B. subtilis* DAPA aminotransferase provided the clue to overcome this bottleneck. A search was made for the real amino donor. After testing 26 different amino acids and related compounds, only lysine was found to dramatically stimulate the *in vitro* conversion of KAPA to DAPA by the *B. subtilis* DAPA aminotransferase. In subsequent testing, D- and L-lysine and the lysine analog, (S)-2-aminoethyl-L-cysteine (AEC), were found to function as amino donors with the *B. subtilis* enzyme. Thus, any of these, in any combination, may be used in the invention. Although there are other known aminotransferases that use lysine as an amino donor (Tobin et al., 1991. *J. Bacteriol.* 173:6223-6229; Coque et al., 1991. *J. Bacteriol.* 173:6258-6264; Soda et al., 1968. *Biochemistry* 7:4102-4109; Soda and Misono, 1968, *Biochemistry* 7:4110-4119; Schmidt et al., 1988, *FEMS Microbiol. Lett.* 49:203; Lowe and Rowe, 1986. *Mol. Biochem. Parasitol.* 21:65), no other known DAPA aminotransferase uses lysine. Both the *E. coli* and the *B. sphaericus* BioA enzymes use SAM (Eisenberg et al., *J. Bacteriol.* 108:1135-1140, 1971; Izumi et al., *Agric. Biol. Chem.* 45:1983-1989, 1981; Stoner et al., *J. Biol. Chem.* 250:4037-4043, 1975; Stoner et al., *J. Biol. Chem.* 250:4029-4036).

Characterization of the *B. subtilis* DAPA aminotransferase indicated that the  $K_m$  for lysine was high and, it was substrate inhibited by KAPA. We conclude that the KAPA to DAPA bottleneck was caused by insufficient lysine or an unfavorable ratio of KAPA/lysine, and that the addition of lysine to the fermentation medium could overcome the block.

When fermented with added lysine (6 g/l), as well as pimelic acid (1 g/l), the engineered *B. subtilis* strain BI282 (bio::[P<sub>15</sub>bio]<sub>7-8</sub>) showed a dramatic increase (>10-fold) in

DTB production. Under these fermentation conditions, BI282 produced about 300-700 mg/l of DTB. Depending on the exact fermentation medium and conditions, nearly all of the KAPA could be converted to DTB. Also, fermentation of strain

5 BI90, a derivative of BI282 that contains a single-copy cassette with the *E.coli bioA* gene transcribed by the *veg* promoter of *B. subtilis* and translated from a synthetic *B. subtilis* ribosome binding site (P<sub>veg</sub>bioA<sub>ec</sub> cassette) in the presence of 6 g/l lysine, 3 g/l methionine (since the *E.*

10 *coli* DAPA aminotransferase uses SAM and methionine is the precursor of SAM), and 1 g/l pimelic acid resulted in >90% conversion of KAPA to DTB and high levels of DTB production, 600-900 mg/l. Bioautography was used to confirm the absence of measurable amounts of KAPA. These data indicate that

15 KAPA accumulation is at least partially caused by insufficient intracellular levels of the amino donor in fermentations with added pimelic acid. Increasing the concentration of lysine in the medium overcomes the KAPA to DAPA bottleneck and results in a significant improvement in

20 DTB production.

Mutations can be introduced into BI282 that deregulate the lysine biosynthetic pathway (see Fig. 4). Fermentation experiments of two lysine analog (AEC) resistant mutants of biotin production strains showed

25 improved DTB titers in the absence of added lysine. However, lysine is still limiting in these mutant strains. Additional mutations need to be added to further deregulate lysine biosynthesis if one wishes to eliminate the lysine feed. Such mutations include those that result in 1)

30 deregulated expression of any or all of aspartokinases I, II, or III, 2) feedback resistant aspartokinases I, II, or III, 3) deregulated expression of diaminopimelate decarboxylase, 4) feedback resistant diaminopimelate

decarboxylase, or 5) any combination of the above (*Bacillus subtilis* and other Gram Positive Bacteria. (1993) A. Sownstein J. Hoch, R. Losick (eds.) pp. 237-267. American Society for Microbiology. Washington, D.C.).

#### 5 **DAPA aminotransferase enzyme assay**

The assay for DAPA aminotransferase is described by Eisenberg and Stoner in 1971 (*J. Bacteriol.* 108: 1135-1140). In this assay, the substrate KAPA is incubated with S-adenosylmethionine (SAM) in the presence of the cofactor pyridoxal 5'-phosphate and cell extract. We measured the amount of DAPA produced in a plate bioassay utilizing an *E. coli* *bioA* strain. Streptavidin (8 µg/ml) was added to the assay mix because extracts of many of the strains to be assayed contained significant amounts of biotin and dethiobiotin which fed the *E. coli* indicator strain used in the bioassay. Contamination by trace amounts of biotin and dethiobiotin was also removed from the KAPA preparation used as substrate by passing the material over an avidin-agarose column. The *E. coli* *bioA*109 strain (MEC1) was used to measure DAPA aminotransferase activity in the bioassay. This *E. coli* *bioA* strain, developed for the assay by Eisenberg, was reported to be many times more sensitive to DAPA than any other *bioA* mutant. Eisenberg's DAPA-sensitive strain was obtained from the *E. coli* Genetic Stock Center at Yale University.

#### ***B. subtilis* DAPA aminotransferase does not utilize SAM as an amino donor.**

A *B. subtilis* strain, BI282, engineered to overexpress *B. subtilis* BioA protein was assayed for DAPA aminotransferase activity: BI282 contains a P<sub>15</sub> *bio* cassette amplified at the *bio* locus (described in Patent Application



0635572A2). A *B. subtilis* strain deleted for the *bio* operon, BI9 ( $\Delta$ bio::*neo*), was included as negative control. DAPA solutions of known concentration were spotted on the bioassay plates so that the amount of DAPA produced in each  
5 assay could be estimated. Measurable DAPA aminotransferase activity was seen in the BI282 extract, but not in the BI9 extract.

The enzyme reaction was approximately linear with time for at least 60 minutes. Using thin layer  
10 chromatography, the product of the reaction was shown to be DAPA. Enzyme activity was destroyed by boiling the extract, or freezing and thawing, although freezing the extract in the presence of 10% DMSO appeared to stabilize the enzyme. Activity was dependent on the presence of KAPA, but  
15 surprisingly, was not dependent on the presence of SAM. However, extracts assayed from *B. subtilis* strains lacking the native *bioA* gene but containing a *bioA* gene derived from either *E.coli* or *S. marcescens*, had DAPA aminotransferase activity dependent on the presence of exogenous SAM. We  
20 conclude that the *B. subtilis* DAPA aminotransferase utilizes a different amino donor than the *E.coli* or *S. marcescens* enzyme. Under the assay conditions used, the specific activity of the *B. subtilis* DAPA aminotransferase was found to be 100-fold lower than that of the *E.coli* or *S.*  
25 *marcescens* enzyme. This low specific activity could be due to limiting concentrations of the amino donor in the extract.

#### **Identification of lysine as an amino donor for *B. subtilis* DAPA aminotransferase**

30 To determine whether *B. subtilis* DAPA aminotransferase activity could be stimulated by addition of other amino donors to the reaction mix, various amino donors

26914-0459  
were screened for their ability to stimulate enzyme activity  
in vitro. A cell free extract prepared from a *B. subtilis*  
strain deleted for the *bio* operon but containing multiple  
copies (4-6) of the *B. subtilis bioA* gene transcribed from a  
5 phage SP01-26 promoter with the cassette integrated at the  
*bpr* locus, BI611 ( $\Delta bio::cat$ ,  $bpr::[P_{26}bioA]_{4-6}$ ), was dialyzed  
to remove any endogenous levels of the amino donor and the  
extract was assayed in the presence of each of the standard  
amino acids and several other amine compounds. Of twenty-  
10 six compounds tested, only L-lysine hydrochloride (>98%  
pure) stimulated DAPA aminotransferase activity (**Table 1**).  
In a subsequent experiment, various lysine derivatives and  
analogues were tested for stimulation of activity (**Table 2**).  
The ability of a more purified preparation of L-lysine (>99%  
15 pure) to stimulate activity supported the conclusion that L-  
lysine is an authentic amino donor for the enzyme and argued  
against the possibility that the true amino donor was a  
contaminant in the lysine preparation. The ability of the  
L-lysine analog, (S)-2-aminoethyl-L-cysteine (AEC), to  
20 stimulate activity further supported the conclusion that L-  
lysine is the true amino donor for *B. subtilis* DAPA  
aminotransferase. The structure of (S)-2-aminoethyl-L-  
cysteine is identical to L-lysine except that the  $\gamma$  carbon  
has been replaced by a sulfur atom.

25 The use of lysine as an amino donor by *B. subtilis*  
DAPA aminotransferase distinguishes the enzyme from other  
bacterial DAPA aminotransferases (from *E. coli*, *S.*  
*marcescens*, and *B. sphaericus*), which use SAM as an amino  
donor.

### 30 **Kinetic studies of *B. subtilis* DAPA aminotransferase.**

The kinetic properties of *B. subtilis* DAPA  
aminotransferase were investigated using a crude cell-free

extract prepared from BI611 ( $\Delta bio::cat$ ,  $bpr::[P_{26}bioA]_{4-6}$ ).

The production of DAPA from KAPA and lysine was shown to be approximately linear with time. The conversion of substrate to product was approximately 10 to 40% in 20 minutes. The

5 total amount of DAPA produced during a standard 20 minute reaction was shown to be directly proportional to the amount of protein added to the reaction mix. The pH optimum for the transamination reaction was determined to be pH 8.6. A linear relationship was demonstrated between KAPA

10 concentration ( $<20 \mu M$ ) and specific activity, when the lysine concentration was kept constant at saturating levels (19mM) (**Figure 1**). Enzyme activity leveled off at KAPA concentrations between  $20 \mu M$  and  $80 \mu M$ , and inhibition of activity was observed at KAPA concentrations above  $80 \mu M$ .

15 Substrate inhibition by KAPA has also been demonstrated for *E. coli* DAPA aminotransferase by Eisenberg and Stoner (1971, *J. Bacteriol.* 108:1135-1140). The *E. coli* enzyme was subject to inhibition by KAPA at levels above  $20 \mu M$ . An approximately linear relationship was demonstrated between  
20 *B. subtilis* bioA enzyme activity and lysine concentration (0-20 mM) when the KAPA concentration was held constant. The enzyme became saturated for lysine at concentrations between 20 and 40 mM.

The substrate inhibition of *B. subtilis* DAPA  
25 aminotransferase by KAPA provides evidence for a double displacement or ping-pong reaction mechanism, as has been shown for *E. coli* DAPA aminotransferase (Stoner et al., *J. Biol. Chem.* 250:4037-4043, 1975). Additional evidence supporting this conclusion is provided by the experiment  
30 presented in **Figure 2**. KAPA concentration was varied at four different fixed lysine concentrations, and initial velocity data was collected and plotted in a double reciprocal form. The lines are approximately parallel in

the region of low KAPA concentration which is indicative of a ping-pong type reaction mechanism (Stoner et al., J. Biol. Chem. 250:4037-4043).

The apparent  $K_m$  values for lysine and KAPA for the  
5 *B. subtilis* DAPA aminotransferase reaction were determined to be in the range of 2-25 mM and 1-5  $\mu$ M, respectively. The  $K_m$  of *E. coli* DAPA aminotransferase for KAPA was previously estimated to be 1.2  $\mu$ M by Stoner and Eisenberg (1975, J. Biol. Chem. 250:4037-4043). The  $K_m$  for lysine was difficult  
10 to measure accurately because KAPA is a substrate inhibitor which presumably competes with lysine for binding to the active site at low lysine concentrations. Nevertheless, the apparent  $K_m$  of *B. subtilis* DAPA aminotransferase for lysine (2-25 mM) was significantly higher than the  $K_m$  of the  
15 purified *E. coli* enzyme for SAM (0.2 mM), as determined by Stoner and Eisenberg (1975, J. Biol. Chem. 250:4037-4043). While not wishing to be bound by a particular mechanism, it appears that the *B. subtilis* DAPA aminotransferase has a relatively high  $K_m$  for lysine, and that, in production  
20 strains which accumulate large amounts of KAPA, the *B. subtilis* DAPA aminotransferase is limited for lysine.

**Fermentations of strains with enhanced *B. subtilis*, *E. coli*, or *S. marcescens* DAPA aminotransferase activity.**

To test whether fermentations of the engineered  
25 biotin production strains were limited for the appropriate amino donors, a series of experiments were done in which lysine, methionine (the precursor to SAM), or lysine plus methionine were fed to fermentations of strains containing the appropriate *bioA* cassette and the level of KAPA-to-DAPA  
30 conversion was measured by vitamer bioassays and bioautography. These experiments were based in part on the hypothesis that the amino donor for the DAPA

aminotransferase became limiting during fermentation resulting in a build-up of KAPA.

5 All fermentations were carried out in computer controlled 14 liter Chemap fermentors utilizing a dissolved oxygen control, glucose-limited fed-batch fermentation strategy. The fermentations were performed using medium described in **Appendix 1**. Pimelic acid, lysine, and methionine were also batched and fed in the fermentations as indicated. The HABA-avidin displacement assay was used to  
10 determine the total amount of dethiobiotin and biotin in shake flask and fermentation samples. Coupling this chemical assay with bioassays (as described in EP 635572, and Tanaka et al., J. Micro. Methods 6:237-247, 1987) that determine biotin levels allows an additional determination  
15 of dethiobiotin production.

The HABA-avidin displacement assay is based on two facts: 1) HABA absorbs more strongly at 500 nm when bound to avidin than when free in solution and 2) DTB or biotin will quantitatively displace HABA from avidin. The description  
20 of this assay is presented as **Appendix 2**. The HABA assay is linear from 2 to 14 mg/l of dethiobiotin (DTB).

Total vitamers were measured as DTB equivalents in fermentation samples that had been acidified before autolaving to prevent KAPA breakdown. Total vitamers were  
25 determined as described in EP 0635572A2.

#### **Lysine-fed fermentation of strains with enhanced *B. subtilis* bioA activity.**

The effect of lysine feed on KAPA-to-DAPA production was studied by using strains, BI282 and BI603, that  
30 overexpress *B. subtilis* DAPA aminotransferase. BI282 overexpresses all biotin biosynthetic genes on a multicopy cassette ( $P_{15}bio$ ), integrated at the *bio* locus. BI603 is a

derivative of BI282 containing multiple copies of an additional *bioA* cassette ( $P_{26}bioA$ ) integrated at the *bpr* locus which further increases the levels of DAPA aminotransferase. **Table 3 (top)** shows the optical densities, biotin and vitamers production of BI603 and BI282 grown with 1 g/l pimelic acid and 6 g/liter lysine in both the batch and feed. The total vitamers produced by BI603 and BI282 with lysine in the batch and feed were about 1300 mg/l and 1000 mg/l, respectively. The biotin production of the three fermentations were comparable (20-22 mg/l). The levels of HABA vitamers (biotin + DTB) in lysine-batched fermentations were sharply higher compared to previous fermentations without lysine. Typically BI282 and BI603 produced between 20-40 mg/liter HABA vitamers. Addition of lysine increased HABA vitamers production of BI603 to 570 mg/l and BI282 to 330 mg/l. Based on the biotin titers, most of the HABA vitamers produced from lysine feeding appeared to be in the form of dethiobiotin. Since biotin is formed from dethiobiotin, the HABA titer represents the total production level of dethiobiotin in the cells (for simplicity dethiobiotin production and HABA vitamers titers will henceforth be used interchangeably). Bioautographies of 30 hour fermentation samples of BI603 confirmed the accumulation of dethiobiotin and showed that DAPA was not accumulated in large quantities (approximately 10 mg/l).

***Methionine-fed fermentation of strains with enhanced E. coli or S. marcescens BioA activity.***

The effect of methionine feed, the precursor to SAM, on the conversion of KAPA-to-DAPA was studied by fermentation of strains BI90 and BI96, expressing the *E. coli* or *S. marcescens* ATCC 31809 DAPA aminotransferase

enzymes, respectively. BI90 (*bio*::[*P*<sub>15</sub>*bio*]<sub>7-8</sub>  
*sacB*::[*P*<sub>veg</sub>*bioA*<sub>ec</sub>]<sub>1</sub>) and BI96 (*bio*::[*P*<sub>15</sub>*bio*]<sub>7-8</sub> *sacB*::[*P*<sub>veg</sub>*bioA*<sub>sm</sub>]<sub>1</sub>)  
 are derivatives of BI282 that contain a single-copy *E. coli*  
*P*<sub>veg</sub>*bioA*<sub>ec</sub> or *S. marcescens* *P*<sub>veg</sub>*bioA*<sub>sm</sub> cassette, respectively,  
 5 integrated at the *sacB* locus. 1 g/l pimelic acid and 3 g/l  
 methionine were added to both the batch and feed; exogenous  
 lysine was not added to these fermentations in order observe  
 the effect on KAPA-to-DAPA conversion by only the gram-  
 negative DAPA aminotransferases. As a negative control,  
 10 BI282, which does not contain an engineered gram-negative  
*bioA* gene, was also grown under identical conditions. As  
 shown in **Table 4**, total vitamer production of BI90, BI96,  
 and BI282 was similar. Biotin production was slightly lower  
 than usual (5-10 mg/l). The levels of HABA vitamers (biotin  
 15 + DTB) in the methionine-fed fermentations of BI90 and BI96  
 were higher than the control BI282 fermentation. BI96  
 expressing the *S. marcescens* ATCC 31809 *P*<sub>veg</sub>*bioA*<sub>sm</sub> cassette  
 produced 3-4-fold more HABA vitamers than BI282. BI90  
 expressing the *E. coli* *P*<sub>veg</sub>*bioA*<sub>ec</sub> cassette produced 5-6 fold  
 20 higher levels of HABA vitamers. As with the previous  
 lysine-fed fermentation of strains expressing the engineered  
*B. subtilis bioA* gene, most of the HABA vitamers were  
 dethiobiotin. Addition of methionine to fermentation of  
 strains with enhanced *E. coli* or *S. marcescens* DAPA  
 25 aminotransferase activity reduced the KAPA-to DAPA block  
 presumably by increasing the level of SAM in the cell.  
 Moreover, to the extent that the *B. subtilis* BioA enzyme  
 synthesized from the engineered *P*<sub>15</sub>*bio* operon in these  
 strains is limited by insufficient lysine, conversion of  
 30 KAPA-to-DAPA may increase when both lysine and methionine  
 are fed to fermentations of BI90 or BI96.

**Lysine and methionine-fed fermentations of strains with enhanced *B. subtilis* and *E. coli* BioA activities.**

The effect of combining both lysine and methionine, the precursor for SAM, on the conversion of KAPA-to-DAPA in fermentations of a strain, BI90, expressing both the *E. coli* and *B. subtilis* DAPA aminotransferases, was studied by adding 1 g/l pimelic acid, 6 g/l lysine, and 3 g/l methionine to both the batch and feed. As control fermentations, BI603 was grown with or without 6 g/l lysine in the batch and feed. As shown in **Table 5A**, BI603 without added lysine produce little HABA vitamers (30 mg/l) of which about 10 mg/l was dethiobiotin. However, with the addition of lysine, dethiobiotin production in BI603 increased more than 10-fold (510 mg/l). Moreover, fermentation of BI90 with both lysine and methionine resulted in almost two-fold more dethiobiotin (930 mg/l) than fermentation of BI603 with lysine alone. The range of dethiobiotin production in BI90 fermentations with lysine and methionine and 1 g/l pimelic acid was about 600-900 mg/l, but in all cases the majority of the KAPA was converted to DTB.

The level of KAPA remaining in these strains was confirmed by analyzing the 30 hour fermentation samples by bioautography using *E. coli*  $\Delta$ bioH as the indicator (**Figure 3 and Table 5B**). In a separate bioautography using *E. coli* MEC1 indicator, DAPA was not detected in large quantities (15 mg/l for BI90 with lysine and methionine and 40 mg/l for BI603 with lysine; **Table 6, bottom**), consistent with earlier lysine-fed fermentations of BI603 (**Table 3, bottom**).

**Lysine-fed fermentations of strains with enhanced *B. subtilis* DAPA aminotransferase activity grown in Amberex based medium.**



We examined the effect of different amounts of added lysine on biotin, DTB (HABA vitamers) and vitamer production in BI282 grown in fermentation medium with Amberex instead of VY (**Table 6**). Under these fermentation conditions, the addition of lysine at 7.5 g/l in batch and feed was sufficient to yield approximately 100% conversion of KAPA to DTB. Addition of higher levels of lysine in the feed (24.8 g/l) did not appear to be required. Fermentations with added lysine and pimelic acid produced about 10-fold more DTB (660-780 mg/l) than a fermentation of BI282 without lysine (60 mg/l). The fermentation without lysine produced 2-3 fold more biotin (12 mg/l) than fermentations with 10-fold higher levels of DTB (4-5 mg/l biotin).

#### ***Construction of BI282 derivatives that overproduce lysine.***

We have also tried to increase the cell's lysine pool by an alternative method, namely boosting the internal lysine biosynthesis capacity. Strains of *Brevibacter* and *Corynebacter* have been developed to product about 80 g/l lysine, so it should be possible to engineer *B. subtilis* to overproduce lysine to the extent necessary to stimulate DTB synthesis. There are two basic approaches to take, 1) collect known mutants that are deregulated for lysine biosynthesis and move the relevant mutations into a biotin producing strain, and 2) isolate mutants deregulated for lysine production by selecting for lysine analog resistance directly in a biotin producing strain background.

#### ***Known lysine deregulated mutants of *B. subtilis*.***

The biosynthetic pathway from aspartate to lysine for *B. subtilis* is outlined in **Figure 4**. The two regulated steps are the first step, catalyzed by aspartokinase, and the last step, which incidentally is the first step

committed solely to lysine, catalyzed by diaminopimelate (DAP) decarboxylase. Both steps are regulated by feedback inhibition and at the level of gene expression. A summary of the regulated enzymes is given in **Table 7**.

5 Four types of mutations leading to deregulated lysine synthesis are known, 1) a DAP resistant aspartokinase I, 2) a constitutive aspartokinase II, 3) a lysine resistant DAP decarboxylase, and 4) an undefined S-2-aminoethyl-L-cysteine (AEC) resistant mutation that is unlinked to any of  
10 the known lysine genes. These known mutations are summarized in **Table 7**. The last three all have an AEC resistant phenotype, and so each could be moved into a biotin production strain by transduction, transformation, or congression.

15 ***Isolation of lysine overproducers directly in biotin producing strain background.***

Three out of the four classical cases of lysine deregulated mutants were isolated by selecting for lysine analog resistance. *B. subtilis* strains, PY79 (Youngman et  
20 al., Plasmid 12:1-9, 1984), BI282, and BI603 were tested for sensitivity to four lysine analogs, on minimal medium with no additive, with threonine, or with DAP plus threonine. The purpose of the additives was to focus the selection on the *lysC* gene, that encodes the lysine sensitive  
25 aspartokinase II. The only analog that inhibited growth under any conditions was AEC. All three strains behaved similarly; all were sensitive to AEC in all three media.

Spontaneous AEC resistant mutants were isolated from PY79, BI282, and BI603. The mutations in these strains are  
30 most likely to be *lysC* constitutive mutants, because according to the literature, most AEC resistance mutants are of that type. Eleven mutants from each parent were tested

for lysine secretion in a minimal medium. The assay used was a biological assay using *B. subtilis* 1A615 (*trpC2 lys::Tn917*) as an indicator strain. None of the parent strains secreted lysine detectable by the assay (<2 mg/l).

5 However, 10 out of 11 PY79 mutants secreted lysine in the range of 20 to 70 mg/l, one BI282 mutant secreted 30 mg/l and one BI603 mutant secreted 26 mg/l lysine. The BI282 and BI603 mutants, called BI641 and BI642, were then tested for biotin production in the fermentor without a lysine feed and  
10 compared to BI282 with a lysine feed. As shown in **Tables 5, 6, and 8**, BI641 and BI642 produced a higher level of DTB than the respective parent strains in the absence of lysine, but not as much as when 6 g/l lysine was fed. Lysine biosynthesis can be further deregulated by introducing a  
15 second lysine deregulating mutation as described above.

#### *Deposit statement*

The subject cultures listed below are deposited under conditions that assure that access to the cultures will be available during the pendency of the patent  
20 application disclosing them to one determined by the Commissioner of Patents and Trademarks to be entitled thereto under 37 C.F.R. 1.14 and 35 U.S.C. 122. The deposits are available as required by foreign patent laws in countries wherein counterparts of the subject application,  
25 or its progeny, are filed. However, it should be understood that the availability of a deposit does not constitute a license to practice the subject invention in derogation of patent rights granted by governmental action.

Further, the subject culture deposits will be stored  
30 and made available to the public in accord with the provisions of the Budapest Treaty for the Deposit of Microorganisms, i.e., they will be stored with all the care

necessary to keep them viable and uncontaminated for a period of at least five years after the most recent request for the furnishing of a sample of the deposits, and in any case, for a period of at least 30 (thirty) years after the date of deposit or or the enforceable life of any patent which may issue disclosing the cultures plus five years after the last request for a sample from the deposit. The depositor acknowledges the duty to replace the deposits should the depository be unable to furnish a sample when requested, due to the condition of the deposits. All restrictions on the availability to the public of the subject culture deposits will be irrevocably removed upon the granting of a patent disclosing them.

15	<u>Strain</u>	<u>ATCC No.</u>
	BI 90	
	BI 96	
20	BI 603	
	BI 641	
25	BI 642	

Other embodiments are within the following claims.

What is claimed is:

- 1           1.    A method of producing a biotin vitamer by:  
2           (a)   culturing a bacterium comprising a lysine-  
3   utilizing DAPA aminotransferase, said culturing taking place  
4   in an environment enriched for lysine, a lysine analog, or a  
5   lysine precursor; and  
6           (b)   recovering said biotin vitamer.

- 1           2.    A method of producing a biotin vitamer by:  
2           (a)   culturing a bacterium comprising a lysine-  
3   utilizing DAPA aminotransferase, wherein said bacterium is  
4   deregulated with respect to lysine production; and  
5           (b)   recovering said biotin vitamer.

- 1           3.    The method of claim 1 in which the bacterium is  
2   engineered to overproduce a lysine-utilizing DAPA  
3   aminotransferase.

- 1           4.    The method of claim 2 in which the bacterium is  
2   engineered to overproduce a lysine-utilizing DAPA  
3   aminotransferase.

- 1           5.    The method of claim 2 or claim 4, wherein  
2   lysine, a lysine analog, or a lysine precursor is  
3   exogenously added to the culture.

- 1           6.    The method of claim 1, claim 2, claim 3, or  
2   claim 4, in which lysine, a lysine analog, or a lysine  
3   precursor is exogenously added to the culture and totals at  
4   least 10 mmoles per liter of culture.

1           7. The method of claim 1, claim 2, claim 3, or  
2 claim 4, in which the biotin vitamer is biotin,  
3 dethiobiotin, or diaminopelargonic acid (DAPA).

1           8. The method of claim 1, claim 2, claim 3, or  
2 claim 4, in which the biotin vitamer is dethiobiotin, and,  
3 after recovering the dethiobiotin, the method further  
4 comprises converting the recovered dethiobiotin to biotin by  
5 a separate fermentation, biochemical reaction, or chemical  
6 reaction, and recovering biotin.

1           9. The method of claim 1, claim 2, claim 3, or  
2 claim 4, in which the bacterium is resistant to a lysine  
3 analog.

1           10. The method of claim 9, wherein said analog is  
2 S-2-aminoethyl-L-cysteine (AEC).

1           11. The method of claim 1 or claim 2, in which the  
2 bacterium is deregulated with respect to at least one biotin  
3 synthetic pathway step in addition to *bioA* expression.

1           12. The method of claim 1, claim 2, claim 3, or  
2 claim 4, in which the biotin vitamer is biotin, and the  
3 method comprises recovering and purifying the biotin.

1           13. The method of claim 1, claim 2, claim 3, or  
2 claim 4, wherein said bacterium is further engineered to  
3 produce a SAM-utilizing DAPA aminotransferase.

1           14. The method of claim 13 in which methionine, S-  
2 adenosylmethionine (SAM), or an analog of SAM is added to  
3 the culture.

1           15. The method of claim 13 wherein lysine, a lysine  
2 analog, or a lysine precursor is added to the culture.

1           16. The method of claim 14, wherein lysine, a  
2 lysine analog, or a lysine precursor is added to the  
3 culture.

1           17. The method of claim 15 in which lysine or a  
2 lysine analog exogenously added to the culture totals at  
3 least 10 mmoles per liter of culture.

1           18. The method of claim 16 in which lysine or a  
2 lysine analog exogenously added to the culture totals at  
3 least 10 mmoles per liter of culture.

1           19. The method of claim 13 in which the biotin  
2 vitamer is biotin, dethiobiotin, or diaminopelargonic acid  
3 (DAPA).

1           20. The method of claim 13 in which the biotin  
2 vitamer is dethiobiotin, and, after recovering the  
3 dethiobiotin, the method further comprises converting the  
4 recovered dethiobiotin to biotin by a separate fermentation,  
5 biochemical reaction, or chemical reaction, and recovering  
6 biotin.

1           21. The method of claim 13 in which the bacterium  
2 is deregulated with respect to at least one biotin synthetic  
3 pathway step other than *bioA* expression.

1           22. The method of claim 13 in which the biotin  
2 vitamer is biotin, and the method comprises recovering and  
3 purifying the biotin.

1           23. A bacterium engineered to overproduce a lysine-  
2 utilizing DAPA aminotransferase and a SAM-utilizing DAPA  
3 aminotransferase.

1           24. The bacterial strains BI90 (ATCC \_\_\_\_ ) and BI96  
2 (ATCC \_\_\_\_ ).

1           25. The bacterium of claim 23, wherein the strain  
2 is further engineered to overproduce the biotin vitamer by  
3 engineered deregulation of at least one biotin synthetic  
4 step, in addition to *bioA* expression.

1           26. The bacterial strain BI603 (ATCC \_\_\_\_ ).

1           27. A bacterium engineered to overproduce a lysine-  
2 utilizing DAPA aminotransferase, wherein the bacterium is  
3 further engineered to overproduce lysine.

1           28. The bacterial strain BI641 (ATCC \_\_\_\_ ) or BI642  
2 (ATCC \_\_\_\_ ).

1           29. A biotin vitamer manufactured by the method of  
2 claim 1, claim 2, claim 3, or claim 4.

1           30. A biotin vitamer manufactured by the method of  
2 claim 13.

1           31. A biotin vitamer manufactured by the method of  
2 claim 14.



OVERCOMING DAPA AMINOTRANSFERASE  
BOTTLENECKS IN BIOTIN VITAMERS BIOSYNTHESIS

Abstract of the Disclosure

A method is disclosed for the increased production of biotin and the biotin precursor dethiobiotin using a bacterium that produces a lysine-utilizing DAPA aminotransferase. The method involves the use of a bacterium that is either grown in the presence of lysine or deregulated for lysine biosynthesis.

226912.B11

COMBINED DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled OVERCOMING DAPA AMINOTRANSFERASE BOTTLENECKS IN BIOTIN VITAMERS BIOSYNTHESIS, the specification of which

☒ is attached hereto.

☐ was filed on \_\_\_\_\_ as Application Serial No. \_\_\_\_\_  
and was amended on \_\_\_\_\_.

☐ was described and claimed in PCT International Application No. \_\_\_\_\_  
filed on \_\_\_\_\_ and as amended under PCT Article 19 on \_\_\_\_\_.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose all information I know to be material to patentability in accordance with Title 37, Code of Federal Regulations, §1.56.

I hereby appoint the following attorneys and/or agents to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith: John W. Freeman

Address all telephone calls to John W. Freeman at telephone number 617/542-5070.

Address all correspondence to John W. Freeman, Fish & Richardson P.C., 225 Franklin Street ,  
Boston, MA 02110-2804.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patents issued thereon.

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FIGURE 1

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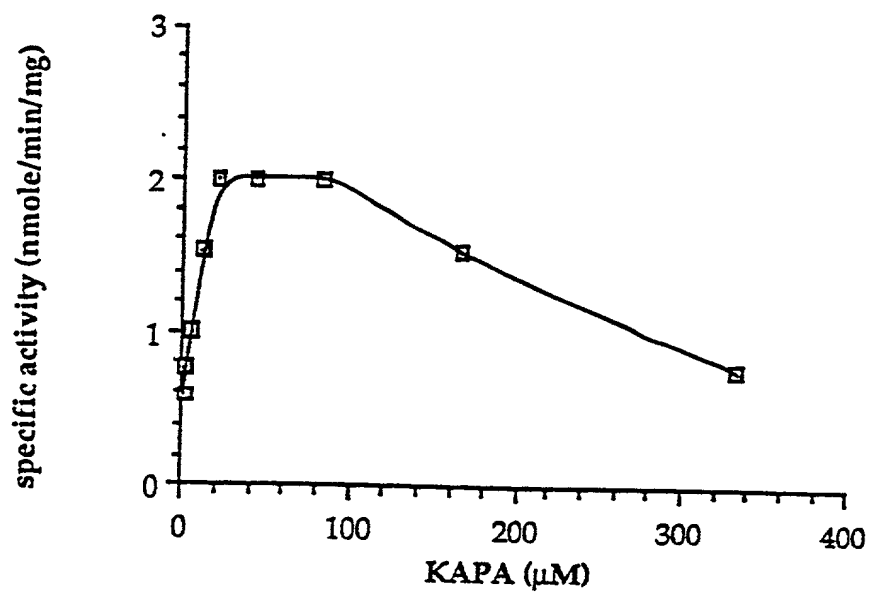


FIGURE 2

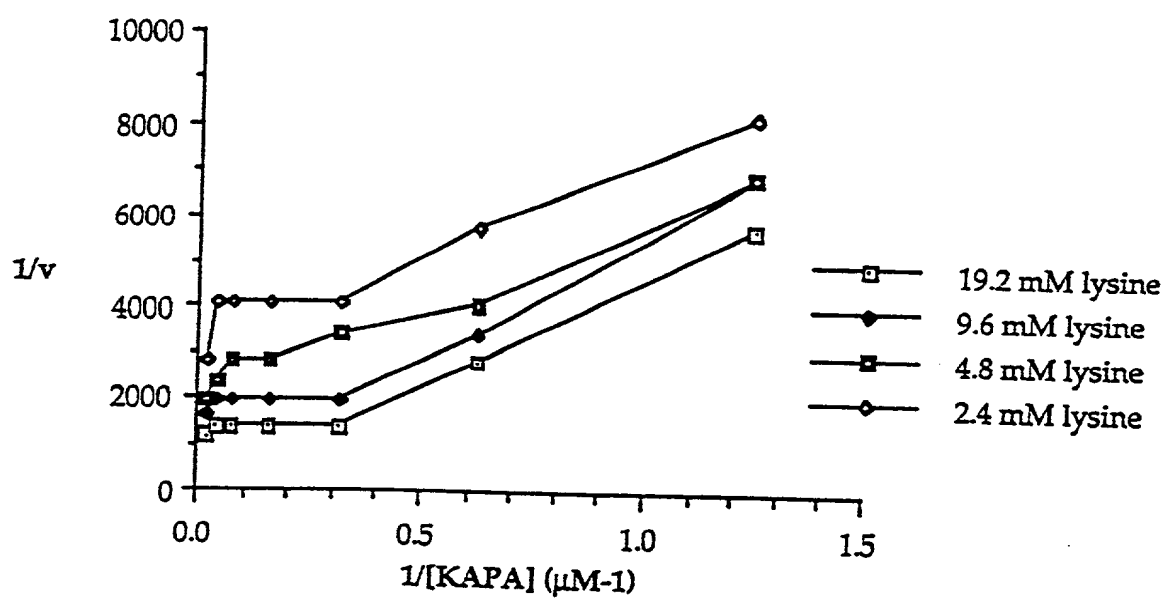
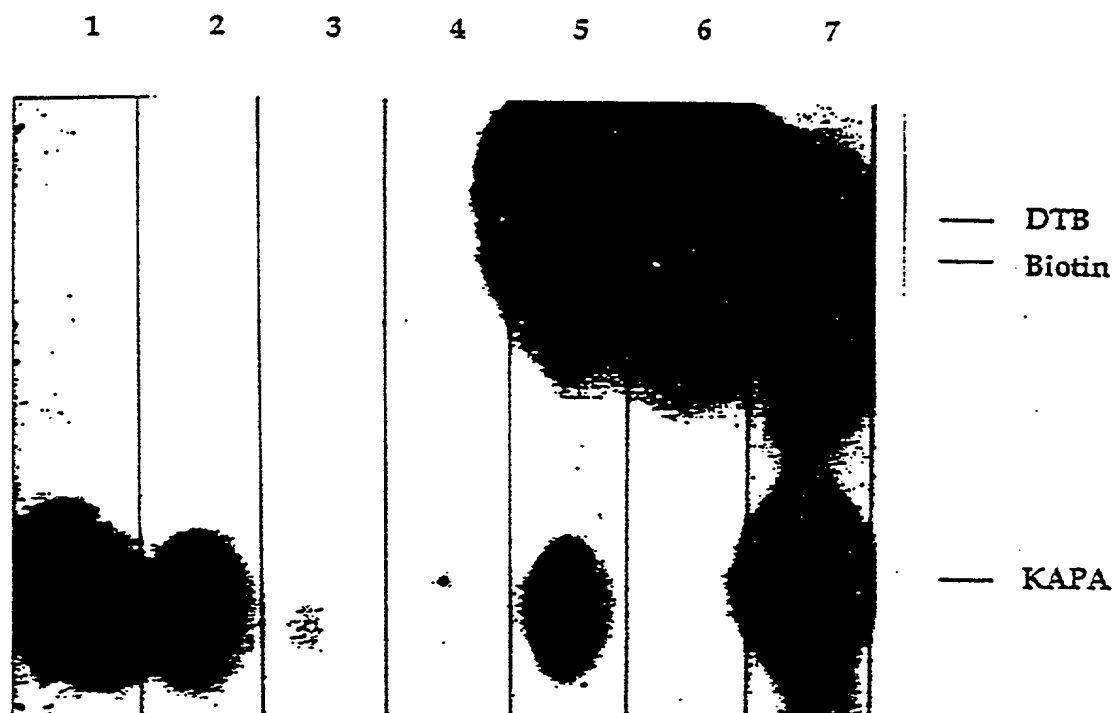


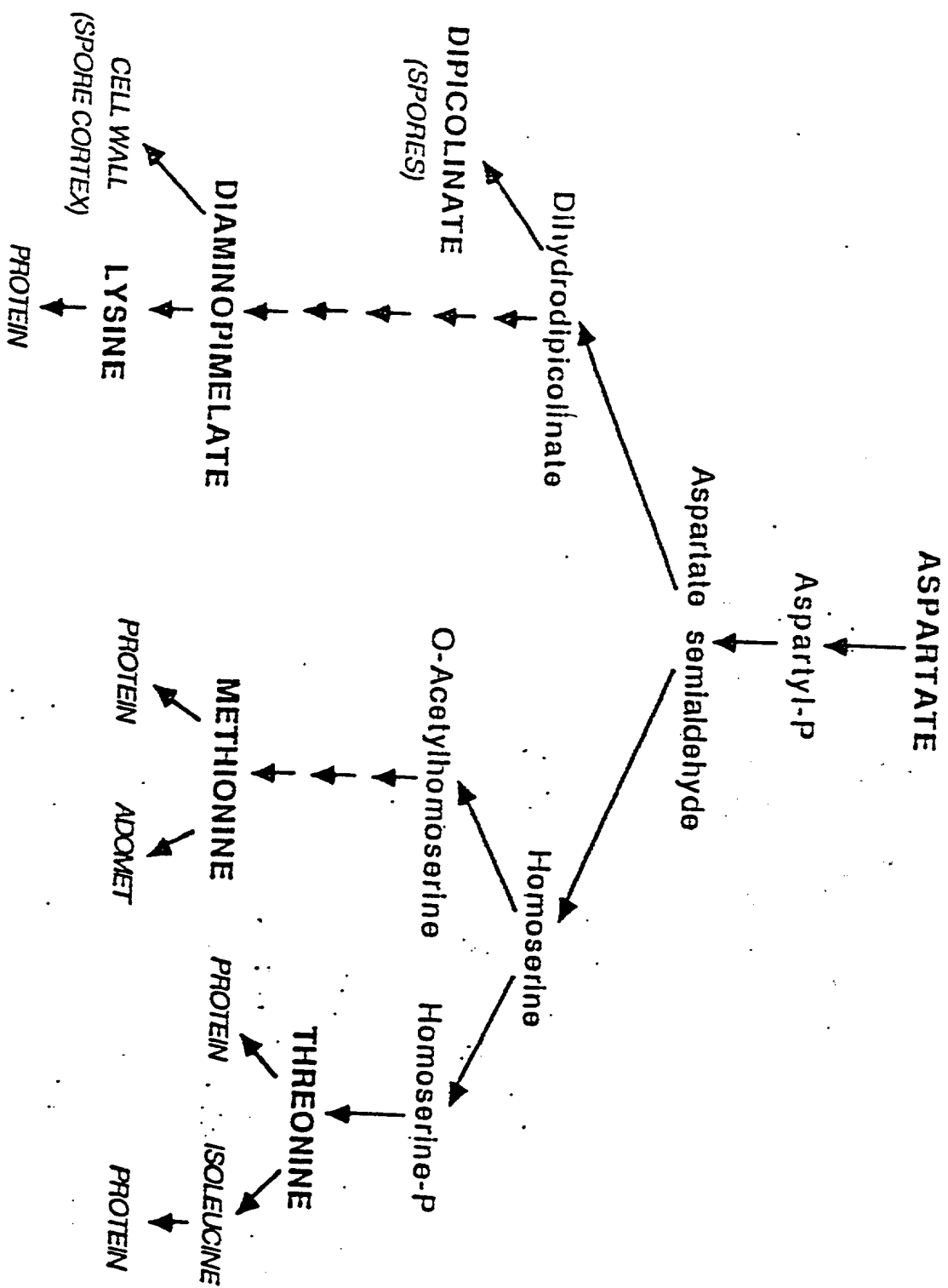
FIGURE 3



<u>Lane</u>	<u>Sample</u> (acid unautoclaved)	<u>Amount</u>
1	KAPA - 0.33 mM/63 mg/L	1 $\mu$ l
2	KAPA - 0.13 mM/25 mg/L	1 $\mu$ l
3	KAPA - 0.07 mM/12 mg/L	1 $\mu$ l
4	KAPA - 0.03 mM/6 mg/L	1 $\mu$ l
5	B167 - 30 hr	1 $\mu$ l - 1/10 dil.
6	B168 - 30 hr	1 $\mu$ l - 1/10 dil.
7	B166 - 30 hr	1 $\mu$ l - 1/5 dil.

<sup>a</sup> DAPA spot not shown.

FIGURE 4



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**APPENDICES**

**FOR**

**UNITED STATES LETTERS PATENT**

**TITLE: OVERCOMING DAPA AMINOTRANSFERASE BOTTLENECKS  
IN BIOTIN VITAMERS BIOSYNTHESIS**

**APPLICANT: SCOTT W. VAN ARSDELL, R. ROGERS YOCUM, JOHN B.  
PERKINS, and JANICE G. PERO**

**2 PAGES OF APPENDICES**

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Appendix I. Medium composition for biotin and vitamins production in bench scale fermentors.

Medium Component	Batch	Concentration	Feed
Glucose	15.0 g/liter	750 g/liter	
Veal Infusion Broth <sup>1</sup>	25.0 g/liter	---	
Yeast Extract <sup>1</sup>	5.0 g/liter	---	
Sodium Glutamate	5.0 g/liter	---	
KH <sub>2</sub> PO <sub>4</sub>	7.5 g/liter	13.7 g/liter	
MgCl <sub>2</sub> ·6H <sub>2</sub> O	1.0 g/liter	1.5 g/liter	
(NH <sub>4</sub> ) <sub>2</sub> SO <sub>4</sub>	2.0 g/liter	---	
MAZU DF-37C	2.5 g/liter	---	
CaCl <sub>2</sub> ·2H <sub>2</sub> O	1.0 g/liter	---	
CuSO <sub>4</sub> ·5H <sub>2</sub> O	0.4 mg/liter	4.0 mg/liter	
ZnSO <sub>4</sub> ·7H <sub>2</sub> O	0.5 mg/liter	5.0 mg/liter	
MnSO <sub>4</sub> ·H <sub>2</sub> O	25.0 mg/liter	35.0 mg/liter	
CoCl <sub>2</sub> ·6H <sub>2</sub> O	1.0 mg/liter	10.0 mg/liter	
Sodium Molybdate-2H <sub>2</sub> O	0.2 mg/liter	2.0 mg/liter	
FeSO <sub>4</sub> ·7H <sub>2</sub> O	50.0 mg/liter	100.0 mg/liter	
Sodium Citrate-2H <sub>2</sub> O	50.0 mg/liter	100.0 mg/liter	

<sup>1</sup> In Amberex Medium the Veal Infusion Broth and Yeast Extract are replaced with 10 g/l Amberex 695.

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**Appendix II. Protocol of avidin-HABA [2-(4-hydroxyphenylazo) benzoic acid] displacement assay for biotin and dethiobiotin.**

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**Reagents and Solutions:**

Buffer: 0.1 M NaPO<sub>4</sub>, pH 7.0.  
Avidin: From Sigma (Cat # A-9275). Dissolved at 5 mg/ml in Buffer.  
HABA: From Aldrich (Cat # 14,803-2). Dissolved at 0.375 M in water + 1 eq. NaOH.

**Prepare Mix:**

	20 samples	50 samples
Avidin	1 ml	2.5 ml
HABA	0.08 ml	0.2 ml
Buffer	38.9 ml	97.3 ml

**Assay:**

Zero spectrophotometer;

Add 2 ml of Buffer to disposable 5 ml cuvette; record OD<sub>500</sub>.

To read sample:

Place disposable 5 ml cuvette in spectrophotometer.

Add 2 ml of Mix; stir; record OD<sub>500</sub>.

Add sample in 0.1 ml volume; stir; record OD<sub>500</sub>.

**Standards:**

Use 0.1 ml DTB at 2 mg/ml to 14 mg/ml as samples.

Use 0.1 ml Buffer as "zero" point.

**Calculations:**

Calculate  $\Delta OD_{500}$  minus  $\Delta OD_{500}$ .

Plot standards and use curve to determine HABA vitamers from samples.

- Notes:
1. Useful range is 2 to 14 mg/l of biotin + dethiobiotin.
  2. Add mix to cuvette, read OD<sub>500</sub>, and then add sample and mix without removing cuvette from the spectrophotometer.
  3. Best results are obtained when a constant volume is used with a set of samples and standards. Use Buffer to bring all samples to the same volume.

**TABLES**

**FOR**

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TABLE 1

Amino donor tested	Stimulation of activity	Amino donor tested	Stimulation of activity
none	-	L-glutamic acid	-
L-methionine	-	L-lysine	+
L-aspartic acid	-	L-tryptophan	-
L-asparagine	-	L-valine	-
L-tyrosine	-	L-leucine	-
L-cysteine	-	L-alanine	-
L-proline	-	L-isoleucine	-
L-serine	-	L-ornithine	-
L-glycine	-	L-homoserine	-
L-glutamine	-	DL-homocysteine	-
L-threonine	-	spermine	-
L-histidine	-	S-adenosyl-L-methionine	-
L-phenylalanine	-	S-adenosyl-L-homocysteine	-
L-arginine	-		

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TABLE 2

Compound added to extract	DAPA aminotransferase specific activity (nmoles/min/mg)
none	0
L-lysine (>98%)	0.76
L-lysine (>99%)	0.56
D-lysine (>98%)	0.19
DL-lysine (>98%)	0.35
N $\alpha$ -acetyl-L-lysine	0
N $\epsilon$ -acetyl-L-lysine	0
N $\epsilon$ -methyl-L-lysine	0
gly-lys	0
lys-gly	0
(S)-2-aminoethyl-L-cysteine	0.48
diaminopimelic acid	0

TABLE 3

Fermentation #/ Strain	Lysine (6 g/liter)		Time (hr)	OD <sub>600</sub>	Total Vitamers (mg/liter)	Biotin (mg/liter)	HABA Vitamers (mg/liter)	Calculated DTB (mg/liter)
	Batch	Feed						
B160/B1603	+	-	24	150	740	16	330	314
B160/B1603	+	-	30	160	950	22	400	378
B161/B1603	+	+	24	140	1100	14	420	406
B161/B1603	+	+	30	160	1290	20	570	550
B162/B1282	+	+	24	132	1100	10	220	210
B162/B1282	+	+	30	140	1000	22	330	308

**Vitamer Breakdown**

Fermentation #/ Strain	Lysine (6 g/liter)		Time (hr)	KAPA (mg/liter)	DAPAA <sup>a</sup> (mg/liter)	DTB (mg/liter)	Biotin (mg/liter)	Total (mg/liter)
	Batch	Feed						
B161/B1603	+	+	30	710	10	550	20	1290

<sup>a</sup> Estimated from bioautography of a an acid autoclaved sample using *E. coli* MEC1 indicator.

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TABLE 4

Fermentation #/ Strain	Time (hr.)	OD <sub>600</sub>	Total Vitamers (mg/liter)	Biotin (mg/liter)	HABA Vitamers (mg/liter)	Calculated DTB (mg/liter)
BI63/BI90	24	150	760	8	126	118
BI63/BI90	30	160	720	9	145	136
BI64/BI96	24	170	830	9	84	75
BI64/BI96	30	160	850	10	88	78
BI65/BI282	24	140	610	5	17	12
BI65/BI282	30	150	590	6	25	19

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TABLE 5A

Fermentation #/ Strain	Batch and Feed		Time (hr)	OD <sub>600</sub>	Total Vitamins (mg/liter)	Biotin (mg/liter)	HABA Vitamins (mg/liter)	Calculated DTB (mg/liter)
	Lys (6 g/liter)	Met (3 g/liter)						
B166/B1603	-	-	24	150	800	20	30	10
B166/B1603	-	-	30	155	600	21	30	9
B167/B1603	+	-	24	143	800	6	460	454
B167/B1603	+	-	30	166	870	5	510	506
B168/B190	+	+	24	128	800	5	890	885
B168/B190	+	+	30	165	1000	5	930	925

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TABLE 5B

Vitamin Breakdown									
Fermentation #/ Strain	Batch and Feed			KAPA					
	Lys (6 g/liter)	Met (3 g/liter)	Time (hr)	(mg/liter)		DAPAc (mg/liter)	DTB (mg/liter)	Biotin (mg/liter)	Total (mg/liter)
				a	b				
B166/B1603	-	-	30	570	470	0	9	21	600
B167/B1603	+	-	30	320	250	40	505	5	870
B168/B190	+	+	30	55	60	15	925	5	1000

<sup>a</sup> Calculated by subtracting DAPA, DTB, and biotin liters from total vitamins.

<sup>b</sup> Estimated from bioautography of acid autoclaved samples using *E. coli* *AbioH* indicator.

<sup>c</sup> Estimated from bioautography of acid autoclaved samples using *E. coli* MEC1 indicator.

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Run/Strain (Drug)	Lysine (g/liter)		Time (hr.)	OD <sub>600</sub>	Total Vitamins (mg/liter)	HABA Vitamins (mg/liter)	Biotin (mg/liter)	%KAPA to DTB conversion (mg/liter)
	Batch	Feed						
B235/B1282 (CAM60)	7.5	24.8	24 30	107 122	590 830	600 660	4 4	100 89
B236/B1282 (CAM60)	----	----	24 30	123 130	410 450	40 60	11 12	10 13
B237/B1282 (CAM60)	7.5	7.5	24 30	115 124	630 670	780 750	4 5	100 100

\*Batch medium (Amberex) contained 1 g/l pimelic acid and the indicated lysine amount; Feed medium contained 1 g/l pimelic acid and the indicated lysine amount.

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Table 7

<u>Enzyme</u>	<u>Type of Mutation</u>	<u>Gene</u>	<u>Map Location</u>	<u>Inhibitor</u>	<u>Corepressor</u>	<u>Decrease in stationary</u>
Aspartokinase I	DAP <sup>r</sup>	dapG	149	DAP	none known	no
Aspartokinase II	constitutive	lysC	252	lysine	lysine	yes
Aspartokinase III	---	---	---	lysine & threonine	threonine	yes
DAP decarboxylase	lys <sup>r</sup>	lysA	210	lysine	lysine & ?	yes
---	---	aecB	282	---	---	---

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TABLE 8

Fermentation #/ Strain	Lysine (6 g/liter)		Time (hr)	OD <sub>600</sub>	Total Vitamers (mg/liter)	Biotin (mg/liter)	HABA Vitamers (mg/liter)	Calculated DTB (mg/liter)
	Batch	Feed						
B190/B1282	+	+	24	84	240	6	270	264
B190/B1282	+	+	30	125	390	7	360	353
B191/B1641 (B1282 $\alpha$ ec7)	-	-	24	74	470	5	130	125
B191/B1641 (B1282 $\alpha$ ec7)	-	-	30	129	500	6	144	138
B192/B1642 (B1603 $\alpha$ ec11)	-	-	24	86	540	4	160	156
B192/B1642 (B1603 $\alpha$ ec11)	-	-	30	120	560	5	110	105

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